

(Linear) MAP of: Bclga.Seq check: 379 from: 1 to: 2241

Sequence of BCLGA (Green) clones from BaF3 library

1 GAATTGGCAGGAGCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTC 60  
CTTAAGCCGTGCTCGAGGGAGGAGGGAGGAAGGAAGGAAGGAGGGAAAGAGGGAG

61 CCTCCCTCCCTCCAGTCCTCCACCAGGAAACAACCGGATTCCGGATCCGGCTGC 120  
GGAGGGAGGGAGGGAGGGTCAGGAGGTGGCTTTGTTGGCTAAGGCCTAGGGCCGACG

GGCCTGACCCGGCTCCACTCTAGCCGGAGGATGAAAGGCCTCAGCTGGGGCTCCCTGC

121 -----+-----+-----+-----+-----+-----+-----+ 180  
CCGGACTGGCCGAGGTGAGATCGGCCCTCCTACTTCCGGAGTCGACCCCCGAGGGACG

181 CACCAGCACTGGGTCTAAGAGCTGCCATCCAGGCTGGCGCCCGGATGGCGACCCCAAGC -----+ 240  
GTGGTCGTGACCCAGGATTCTCGACGGTAGGTCCGACCGGCGGGCTACCGCTGGGTCTG

241 CTCAACCCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTATAAGCTGAGGCAGAA -----+ 300  
GAGTTGGGTCTGTGTGCCCGAGATCACCAGCTGAAACATCCGATATTGACTCCGTCTT

301 GGGTTATGTCTGTGGAGCTGGCCCTGGGAAGGCCAGCCGCCACCCGCTGCACCAAGC -----+ 360

CCCAATAACAGACACCTCGACCGGGACCCCTTCGGGTGGCGCTGGGCACGTGGTCG

361 CATGCGGGCTGCTGGAGACGAGTTGAGACCCGTTCCGCCGCACCTTCTCTGACCTGGC 420  
-----+-----+-----+-----+-----+-----+-----+-----+  
GTACGCCCGACGACCTCTGCTCAAACCTGGCAAAGGCGGCGTGGAAAGAGACTGGACCG

421 CGCTCAGCTACACGTGACCCCCAGGCTCAGCCAGCAACGCTTCACCCAGGTTCCGACGA 480  
-----+-----+-----+-----+-----+-----+-----+-----+  
GCGAGTCGATGTGCACTGGGTCCGAGTCGGTCTGGTGCAGTGGTCCAAAGGCTGCT

481 ACTTTCCAAGGGGGCCCTAAGTGGGGCGTCTGTGGCATTCTTGTCTTGGGCTGC 540  
-----+-----+-----+-----+-----+-----+-----+-----+  
TGAAAAGGTTCCCCCGGGATTGACCCCCGGCGAACACCGTAAGAACAGAAACCCCGACG

541 CCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTGGTGGGACAAGTGCAGGATTG 600  
-----+-----+-----+-----+-----+-----+-----+  
GGACACACGACTCTCACAGTTGTTCTTACCTCGGAAACCACCCCTGTTCACGTCCTAAC

601 GATGGTGGCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGCAGTGGGGCTGGC 660  
-----+-----+-----+-----+-----+-----+-----+  
CTACCACCGGATGGACCTCTGTGAGACCGACTGACCTAGGTGTCGTACCCCCGACCCG

661 GGAGTTCACAGCTCTACGGGGACGGGGCCCTGGAGGGAGGCACGGCGTCTGCAGGGAGGG 720  
-----+-----+-----+-----+-----+-----+-----+  
CCTCAAGTGTGAGATATGCCCTGCCGGGACCTCCTCCGTGCCGCAGACGCCCTCCC

721 GAACTGGGCATCAGTGAGGACAGTGCTGACGGGGCCGTGGCACTGGGGCCCTGGTAAC 780  
CTTGACCCGTAGTCACTCCTGTCACGACTGCCCGGCACCGTGACCCCCGGGACCATG

781 TGTAGGGGCCTTTTGCTAGCAAGTGAGAAAGTCTAGGGCCAGGTGGGCTAGGTGTGG 840  
ACATCCCCGGAAAAACGATCGTTCACTCTTCAGATCCGGTCCACCCCGATCCACACC

841 CTAGGGGCCAGGAGAGCTGGAACAATAGCGAATGCCCTGGAAAGAAACTGGATGTCACGG 900  
GATCCCCGGTCCTCTGACCTTGTATCGCTTACGGGAACCTTCTTGACCTACAGTGCC

901 ACGAGAGAAAGGCAGGGGAAGGTAGTGTGTGGGAGCCCATCATCCCAGGCAGGTGGCA  
TTGTCTCTTCCGTCCCCTTCATCACACACACCCTCGGGTAGTAGGGTCCGTCCACCGT 960

961 GGGAGAACATTAAGGAATGTTCAAGGCCTAGAACCCAGAGAGTGGAGT  
CCCTCTTACTCAACCTTGTAATTCTTACAAAGTTCCGGATCTGGGTCTCTCACCTCA 1020

1021 CATCCCACGGCTTGGGGGTGGGGAGGTGGGATGAATCATGCCCATATCGCGGG  
GTAGGGTGCCGAACCCCCACCCCCCTCCACCCCTACTTAGTACGGGTATAGCGCCC 1080

1081 CACACAACTACCCGGAACATGGCTTGTAGCTCCCAAGGACGGTGAGCTTACTTCANAGAT  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1140  
GTGTGTTGATGGGCCTTGTACCGAACATCGAGGGTCCCTGCCACTCGAACATGAAGTNTCTA

1141 CTGTGTCTCGACTAGATGAATGGGATTTAGGAGCCTAGAATTCACTTCCCTTGGGATGG  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1200  
GACACAGAGCTGATCTACTTACCCCTAAATCCTCGGATCTTAAGTGAAGGGAAACCCCTACC

1201 AAGCTTGGTGATCAGGTGACTGGGTGAAATGGCTGTGGCTGTGGCTGCATGGCACACC  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1260  
TTCGAACCACTAGTCCACTGACCCACTTTACCGACACCGACACCGACGTACCCGTGTGG

1261 TGTGCATGTATGTGCACATGCAAGCATGCTCATGTGCATGCTGGGCTGTCTGTCGAATCT  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1320  
ACACGTACATACACGTGTACGTTCGTACGAGTACACGTACGACCCGACAGACAGCTTAGA

1321 GGTGGTGGGGTACTTAGAGAAAACATTCCCTTCTGCTATGGCAAGAACAAAGGGGAGTTC  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1380  
CCACCACCCCATGAATCTCTTTGTAAGGAAGAACGATACC GTTCTTGTCCCCGTCAAG

1381 ACTGCCCTTCCTCTCTGCCCTTCCCTTGACCTTACGCCCTCCAGGCTGAGGGAGGAAC  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1440  
TGACGGGAAGAGGAGAGACGGGGAGGGAACTGGAATGCGGAGGTCCGACTCCCTCCTTG

ACTGCATCTAGACTAGGGCTCTGGTGTGCCGAGAGTTGGCAGGGCTTGGGAGAGAA  
1441 -----+-----+-----+-----+-----+-----+-----+-----+ 1500  
TGACGTAGATCTGATCCCGAGACCACGACGGCTCTCAACAACCGTCCGAACCCCTCTTT

GAGTTCTGCAGGTGGCCTTGTCTTCATCATCCCCCTGTGGTGTGCATCTGTGCACCTGG  
1501 -----+-----+-----+-----+-----+-----+-----+-----+ 1560  
CTCAAGACGTCCACCGGAACAAGAAGTAGTAGGGGGACACCACACGTAGACACGTGGACC

GCTGAAAAAGGGTAAAGCTGTGGAGCCTGGTGGTAGAAGCTTGGTAGGTGGGACTTG  
1561 -----+-----+-----+-----+-----+-----+-----+-----+ 1620  
CGACTTTTCCCATTTCGACACCTCGGACCCACCCATTTCGAACCCATCCACCCCTGAAC

GCTGTCACCTCCCCCTCCAACGGGGGG.....  
1621 -----+-----+-----+-----+-----+-----+-----+-----+ 1680

CGACAGTGGAGGGAGGGTTGCC.....

1681 .....CCAGTGGAAACCCAGAGACTCTTCTTCAGGGAGGACCAGGG  
.....GGTCACCTTGGGTCTCTGAGAAGAAAGTCCCTCCCTGGTCCC 1740

1741 CCTTTCTTTAGAGCCATATAGTTCCCTGGGATTAGCTCTGCCAAGAAGGCTGAGTA  
.....GGAAAGAAAATCTCGGTATATCAAGGAAACCTAATCGAGAACGGGTTCTTCCGACTCAT 1800

1801 TGCCTCCCCACCTTTAAATCCATTTCTTTAAATGAGGGAAATGGATATAATT  
.....ACGGAGGGGTGGAAAATTAGGTAAAGTAAAAAAATTACTCCCTTACCTATATTAAA 1860

1861 TTCAGATACTAAGTAGCTGGAGAGGATGTTCTGCTCTCCAAAGCCAAAGGGACAAAT  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1920  
AAGTCTATGATTCATCGACCTCTCTACAAGAACGAGAGGGTTCGGGTTCCCTGTTA

1921 AGGGACTTGTAGGCCAAGGCAAGAGCGAAGTGGGCACTCAGTCCTGCAGTACCAAG  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1980  
TCCCTGAAACGAATCCGGTCCGTTCTCGCGTTCACCCGTGAGTCAGGACGTCAATGGTC

1981 TCCTACTCCCCACTTACACTAGGGCATACATATACTATTTACTTTTAAATCATAACG  
 2040  
 AGGATGAGGGGTGAATGTGATCCGTATGTATGATAAAATGAAAAAATTTAGTATTGC

2041 GCAGGAGAACAGATTGGTTAGTTAGAAGAAAAGGAAACCTCTATAAAATATAAAATATA  
-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2100  
CGTCCTCTTGTCTAACCAATCAAATCTCTTCTTGGAGATTTATTTATAT

2101 TATTCCTGTATTTTATTTAATAATTATAAAATGCCAAGTCATTGACTTTATTTTG  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2160  
ATAAGGACATAAAATAAAATTATAAAATTACGGTCAAGTAAACTGAAAATAAAAAC

2161 TGTAATATGTAATGGTCGTATTAATAAAATAAAAGCCCAGAAATTAAATGAGGAA  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2220  
ACATTATACATTACAGCATAATTATTTATTTATTCGGGTCTTAAATTACTCCTT

2221 AAAAAAAAAAAACTCGAG  
-----+-----+-----+-----+-----+-----+-----+-----+ 2241  
TTTTTTTTTTTTTGAGCTC